

FIGURE 1B: V_H DOMAIN

	10	20	30	40	50	A
4D5	EVQLQQSGPELVKPGASLKL	SCTASGFNIKDTYIHWVKQRPEQGLEWIGRIYPTN				
HU4D5	EVQLVESGGGLVQPGGSLRLS	CAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTN				
HUV _H III	EVQLVESGGGLVQPGGSLRLS	CAASGFTFSDYAMSWVRQAPGKGLEWVA	ISENG			
			-----			-----
			-----			-----
			V _H -CDR1			V _H -CDR2

	60	70	80	ABC	90	100ABC
4D5	GYTRYDPKFQDKATITADTSSNTAYLQVSRLTSED	TAVYYCSRWGGDGFYAMDYW				
HU4D5	GYTRYADSVKGRFTISADTSKNTAYLQMNSLRAED	TAVYYCSRWGGDGFYAMDVW				
HUV _H III	SDTYYADSVKGRFTISRDDSKNTLYLQMNSLRAED	TAVYYCARDRGGGAVSYFDVW				
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						V _H -CDR3

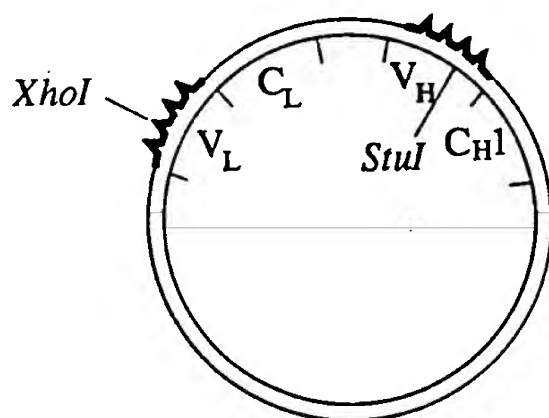
	110
4D5	GQGASVTVSS
HU4D5	GQGTLVTVSS
HUV _H III	GQGTLVTVSS

FIGURE 2

Anneal huV_L or huV_H oligomers to pAK1 template



1. Ligate
2. Isolate assembled oligomers
3. Anneal to pAK1 template ($XhoI^-$, $StuI^+$)
4. Extend and ligate



1. Transform *E. coli*
2. Isolate phagemid pool
3. Enrich for huV_L and huV_H ($XhoI^+$, $StuI^-$)
4. Sequence verify

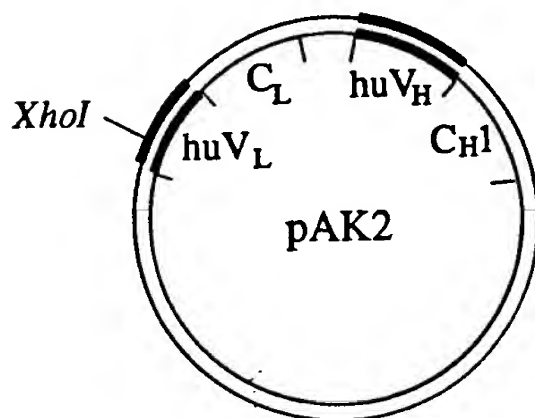


FIGURE 3

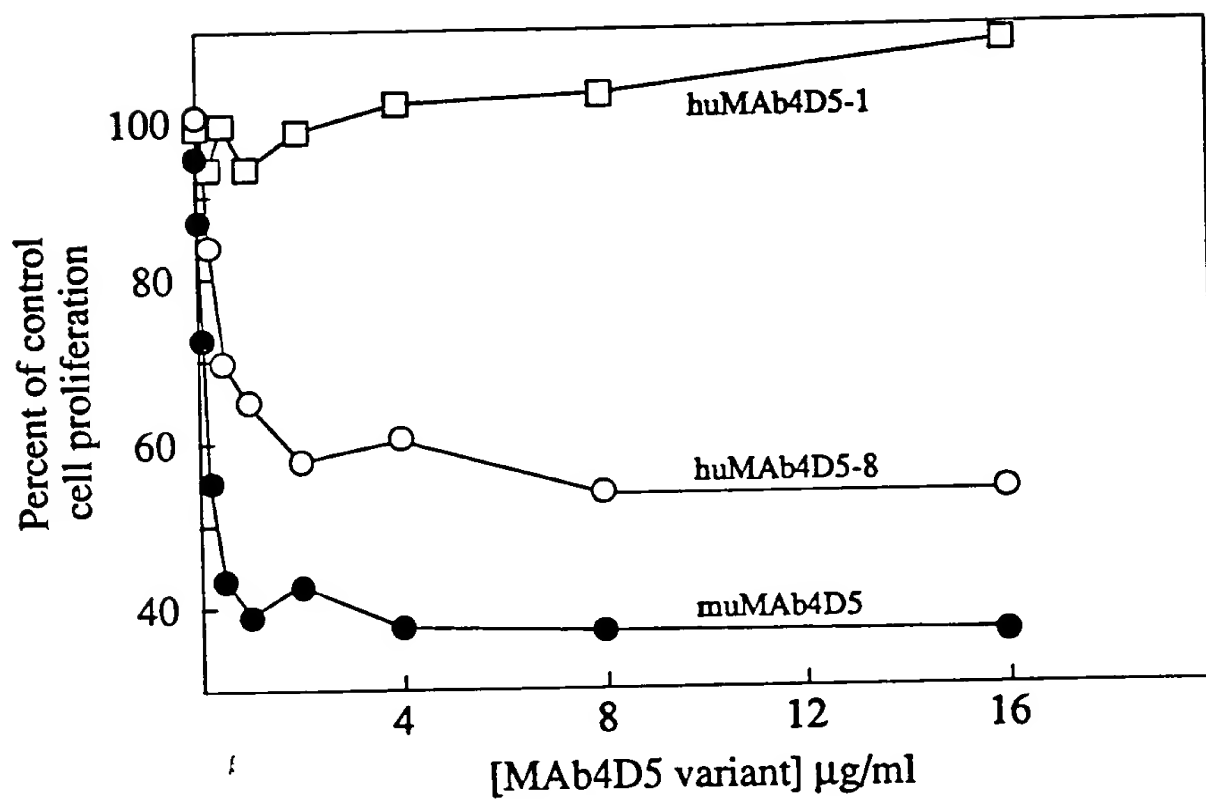


FIGURE 4

